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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/509,648

DATE: 06/28/2001

TIME: 13:59:49

Input Set : A:\Cbm-691.app

Output Set: N:\CRF3\06282001\I509648.raw

3 <110> APPLICANT: Charette, Marc F.
4 Rueger, David C.
5 Higgins, Dennis
7 <120> TITLE OF INVENTION: ENHANCEMENT OF MORPHOGEN ACTIVITY
9 <130> FILE REFERENCE: 00960-569 NATL
11 <140> CURRENT APPLICATION NUMBER: 09/509,648
12 <141> CURRENT FILING DATE: 2000-10-05
14 <150> PRIOR APPLICATION NUMBER: PCT/US98/22655
15 <151> PRIOR FILING DATE: 1998-10-26
17 <150> PRIOR APPLICATION NUMBER: 60/063,624
18 <151> PRIOR FILING DATE: 1997-10-27
20 <160> NUMBER OF SEQ ID NOS: 9
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1822
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (49)..(1341)
33 <400> SEQUENCE: 1
34 ggtgcgggcc cggagcccgc agcccgggta gcgcgtagag ccggcgcg atg cac gtg 57
35 Met His Val
36 1
38 cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105
39 Arg Ser Leu Arg Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
40 5 10 15
42 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
43 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
44 20 25 30 35
46 gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
47 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
48 40 45 50
50 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
51 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
52 55 60 65
54 ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297
55 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
56 70 75 80
58 ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggg ccc ggc 345
59 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
60 85 90 95
62 ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393
63 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
64 100 105 110 115
66 ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac 441
67 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp

ENTERED

See p.5

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68          120          125          130
70 atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc 489
71 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
72          135          140          145
74 cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc 537
75 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
76          150          155          160
78 cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac 585
79 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
80          165          170          175
82 tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat 633
83 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
84 180          185          190          195
86 cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc 681
87 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
88          200          205          210
90 gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac 729
91 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
92          215          220          225
94 atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg 777
95 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
96          230          235          240
98 ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc 825
99 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
100          245          250          255
102 aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc 873
103 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
104 260          265          270          275
106 ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc 921
107 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
108          280          285          290
110 cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc 969
111 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
112          295          300          305
114 aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc 1017
115 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
116          310          315          320
118 agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc 1065
119 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
120          325          330          335
122 cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc 1113
123 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
124 340          345          350          355
126 gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg 1161
127 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
128          360          365          370
130 aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac 1209
131 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
132          375          380          385

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134 ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc 1257
135 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
136          390          395          400
138 atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa 1305
139 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
140          405          410          415
142 tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351
143 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
144 420          425          430
146 gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag 1411
148 gaaccagcag accaactgcc ttttgtgaga ccttcccctc cctatcccca actttaaaagg 1471
150 tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc 1531
152 atccaatgaa caagatccta caagctgtgc aggcaaaacc tagcaggaaa aaaaaacaac 1591
154 gcataaagaa aaatggccgg gccagggtcat tggctgggaa gtctcagcca tgcacggact 1651
156 cgtttccaga ggtaattatg agcgccctacc agccaggcca cccagccgtg ggaggaaggg 1711
158 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagtgc 1771
160 ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaa aaaaaaaaaa a 1822
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 431
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
170 1 5 10 15
172 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
173 20 25 30
175 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
176 35 40 45
178 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
179 50 55 60
181 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
182 65 70 75 80
184 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
185 85 90 95
187 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
188 100 105 110
190 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
191 115 120 125
193 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
194 130 135 140
196 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
197 145 150 155 160
199 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
200 165 170 175
202 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
203 180 185 190
205 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
206 195 200 205
208 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu

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```

209      210      215      220
211 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
212 225      230      235      240
214 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
215      245      250      255
217 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
218      260      265      270
220 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
221      275      280      285
223 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
224      290      295      300
226 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
227 305      310      315      320
229 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
230      325      330      335
232 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
233      340      345      350
235 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
236      355      360      365
238 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
239      370      375      380
241 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
242 385      390      395      400
244 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
245      405      410      415
247 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
248      420      425      430

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252 <210> SEQ ID NO: 3

253 <211> LENGTH: 102

254 <212> TYPE: PRT

255 <213> ORGANISM: Artificial Sequence

257 <220> FEATURE:

258 <223> OTHER INFORMATION: Description of Artificial Sequence: OPX -
 259 Consensus sequence

261 <220> FEATURE:

262 <223> OTHER INFORMATION: Wherein Xaa is independently selected from a group
 263 of one or more specified amino acids as defined in
 264 the specification

266 <400> SEQUENCE: 3

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W--> 267 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
268      1      5      10      15
W--> 270 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
271      20      25      30
W--> 273 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
274      35      40      45
W--> 276 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
277      50      55      60
W--> 279 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
280      65      70      75      80

```

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W--> 282 Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
283 85 90 95

W--> 285 Xaa Ala Cys Gly Cys His
286 100

289 <210> SEQ ID NO: 4
290 <211> LENGTH: 97
291 <212> TYPE: PRT
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic
296 Sequence 7
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Wherein Xaa is independently selected from a group
300 of one or more specified amino acids as defined in
301 the specification
303 <400> SEQUENCE: 4

W--> 304 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa Xaa
305 1 5 10 15

W--> 307 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
308 20 25 30

W--> 310 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
311 35 40 45

W--> 313 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
314 50 55 60

W--> 316 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
317 65 70 75 80

W--> 319 Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
320 85 90 95

W--> 322 Xaa
326 <210> SEQ ID NO: 5
327 <211> LENGTH: 102
328 <212> TYPE: PRT
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic
333 Sequence 8
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Wherein Xaa is independently selected from a group
337 of one or more specified amino acids as defined in
338 the specification
340 <400> SEQUENCE: 5

W--> 341 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
342 1 5 10 15

W--> 344 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
345 20 25 30

W--> 347 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
348 35 40 45

W--> 350 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
351 50 55 60

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Cbm-691.app

Output Set: N:\CRF3\06282001\I509648.raw

L:267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:276 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:276 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:279 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:279 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:282 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:282 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:304 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:304 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:307 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:307 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:310 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:313 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:313 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:316 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:316 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:319 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:319 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:322 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:322 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:341 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:341 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:341 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:344 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:344 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

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L:347 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:347 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:350 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:353 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:353 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:353 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:356 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:356 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:359 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:378 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:378 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:381 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:381 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:384 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:384 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:387 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:387 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9